

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:39:13 ; Search time 1839.23 Seconds
(without alignments)
16145.302 Million cell updates/sec

Title: US-09-645-337-3

Perfect score: 1800

Sequence: 1 gtgccacacactcctagtaa.....acgcgtgcatgagacgtcat 1800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
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16: em_fun:*
17: em_hum:*
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20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1799	99.9	1800	6	AX139016	AX139016 Sequence
2	1732	96.2	1733	8	AF195548	AF195548 Arabidops
3	712.8	39.6	81662	8	AB008265	AB008265 Arabidops
4	615.6	34.2	1742	8	AF045473	AF045473 Zea mays
5	549.6	30.5	1906	8	AF384032	AF384032 Zea mays
6	525.2	29.2	2047	8	AF035815	AF035815 Zea mays
7	523.4	29.1	1807	6	AX139014	AX139014 Sequence
8	523.4	29.1	1807	8	AF195547	AF195547 Arabidops
9	523.4	29.1	1808	8	AF014824	AF014824 Arabidops
10	503.8	28.0	1579	8	AF332875	AF332875 Oryza sat
11	496.2	27.6	1839	8	AF282858	AF282858 Mesembrya
12	462	25.7	2172	3	DMHLSSEAC	Y09258 D.melanogas
13	459.2	25.5	1878	5	AF039752	AF039752 Gallus ga
14	458.6	25.5	2073	3	AF026949	AF026949 Drosophil
15	444.6	24.7	1985	6	AX053103	AX053103 Sequence
16	444.6	24.7	1985	9	HSU31814	U31814 Human trans
17	441.8	24.5	1997	10	MMU31758	U31758 Mus musculu
18	440.4	24.5	2305	5	XLAB21	X78454 X.laevis AB
19	436.6	24.3	1611	6	AX053101	AX053101 Sequence
20	436.6	24.3	1611	9	HSU50079	U50079 Human histo
21	436.6	24.3	2093	9	BC000301	BC000301 Homo sapi
22	435.4	24.2	1977	10	MMHIDE	X98207 M.musculus
23	435	24.2	2091	9	D50405	D50405 Human mRNA
24	435	24.2	2111	6	AR012007	AR012007 Sequence
25	435	24.2	2111	6	162388	162388 Sequence 2
26	435	24.2	2111	22	E11455	E11455 cDNA encodi
27	433	24.1	1999	10	MMU80780	U80780 Mus musculu
28	424.2	23.6	51246	2	AC014151	AC014151 Drosophil
29	424.2	23.6	301769	3	AF003482	AF003482 Drosophil
30	421.8	23.4	41465	8	AB023031	AB023031 Arabidops
31	421.2	23.4	2180	3	AF032919	AF032919 Strongylo
32	421	23.4	1646	5	AF043328	AF043328 Gallus ga
33	421	23.4	1646	5	AF044169	AF044169 Gallus ga
34	421	23.4	1678	5	AF039751	AF039751 Gallus ga
35	420.2	23.3	1487	5	AF020658	AF020658 Xenopus l
36	417.8	23.2	2681	3	AF086715	AF086715 Drosophil
37	403.6	22.4	1645	8	S66438	S66438 RPD3 [Sacch
38	403.6	22.4	2292	8	SCYNL330C	271606 S.cerevisia
39	403.6	22.4	8223	8	SCDNANO	X83226 S.cerevisia
40	403	22.4	2544	8	AY035205	AY035205 Kluyverom
41	383.6	21.3	1437	8	AF377895	AF377895 Candida a
42	379.8	21.1	1920	9	AF039703	AF039703 Homo sapi
43	379.8	21.1	2929	8	UWA133752	AJ133752 Ustilago
44	379.2	21.1	1799	10	AF321131	AF321131 Rattus no
45	378.6	21.0	1975	10	AF074881	AF074881 Mus muscu

ALIGNMENTS

RESULT 1

AX139016

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

PAT 30-MAY-2001

AX139016 1800 bp DNA
Sequence 3 from Patent EP1094112.

AX139016.1 GI:14274699

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 1800)

Wu,K., Miki,B.L., Tian,L. and Brown,D.C.

Repressing gene expression in plants

Patent: EP 1094112-A 3 25-APR-2001;

The Minister of Agriculture and Agri-Food (CA)

Location/Qualifiers

1. .1800

/organism="Arabidopsis thaliana"

BASE COUNT 478 a /db_xref="taxon:3702"
 ORIGIN 389 c 456 g 476 t 1 others

Query Match 99.9% Score 1799; DB 6; Length 1800;
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 Matches 1800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 541 GCTGATATCGCTATCAATTGGGGCGGTGGGCTTCACCATGCTTAAGAAAGCGAGCTTCT 600

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 DB 781 GGTACATAAAGAGATTGTGGCGCTGAAAGAGGAATACTATGCTCTAAATGTTCCACTA 840

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RESULT 2

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 DEFINITION Arabidopsis thaliana putative histone deacetylase (HPD3B) mRNA,
 complete cds.
 ACCESSION AF195548
 VERSION AF195548.1 GI:11066140
 KEYWORDS thale cress.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1733)
 REFERENCE Wu, K., Malik, K., Tian, L., Brown, D. and Miki, B.
 AUTHORS Functional analysis of RPD3 histone deacetylase homologs in

JOURNAL Arabidopsis thaliana
REFERENCE 2 (bases 1 to 1733)
AUTHORS Wu, K., Tian, L., Malik, K., Brown, D. and Miki, B.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1999) Eastern Cereal and Oilseed Research Centre,
 Agriculture and Agri-Food Canada, Ottawa, Ontario K1A 0C6, Canada
FEATURES Location/Qualifiers
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 /cultivar="Columbia"
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 GFCYINDIVLIGLLELLKMKRVLHIDIVRHGDCVEAFYITDRVMTYVSHKGFDFP
 GTGHIRDVGABKYYALNPLNDMDDESFRSLRPLIOKVMVEYQPEAVLQCGAD
 SLSDRLGCFNLGSHADCLRFRLSYNPLVLGGEGYIRINRYACWYETAVAGV
 SPDNKLIYNEFYEGPDYTLHVDPSMELNLTPKDMERIRNTLLEQLSLIHAPSVQ
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 STGDEMDDDNPEPDVNPSS"
 BASE COUNT 453 a 374 c 439 g 466 t 1 others
 ORIGIN

Query Match 96.2% Score 1732; DB 8; Length 1733;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1733; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AB008265/c
LOCUS
DEFINITION
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ACCESSION
AB008265.1 GI:2618600
VERSION
AB008265.1 GI:2618600
KEYWORDS
SOURCE
Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
clone:MDC12.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. III.
Sequence features of the regions of 1,191,918 bp covered by
seventeen physically assigned P1 clones
DNA Res. 4 (6), 401-414 (1997)
98162728
2 (bases 1 to 81662)
Nakamura,Y.
Direct Submission
Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/aggd_graph.cgi?c=MDC12
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlini.zozi.laestate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is M422 and the 3' clone is K9H21.
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QY      659  ----- 658

Db 26202  GCCTTGTGTGATTATCGAATGAGCTTTGATCCTTTCATGTTCCCTTAACTGCATATTACCT 26143

QY      659  ----- 658

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LOCUS Zea mays histone deacetylase (hd1b) mRNA, complete cds.
DEFINITION Zea mays histone deacetylase (hd1b) mRNA, complete cds.
ACCESSION AF045473
VERSION AF045473.1 GI:4193319
KEYWORDS Zea mays.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1742)
Pipal, A. and Wegener, S.
Direct Submission
Submitted (28-JAN-1998) Microbiology-Medical School, University of
Innsbruck, Fritz-Pregl-Strasse 3, Innsbruck A-6020, Austria
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ORIGIN

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RESULT 10

AF332875

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AF332875

1579 bp

mRNA

Oryza sativa histone deacetylase HD1 mRNA, complete cds.

07-FEB-2001

AF332875

AF332875.1

GI:12698879

Oryza sativa.

Oryza sativa

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 1579)

Song,F. and Goodman,R.M.

Molecular characterization of a rice histone deacetylase gene OsHD1

Unpublished

2 (bases 1 to 1579)

Song,F. and Goodman,R.M.

Direct Submission

Submitted (30-DEC-2000) Department of Plant Pathology, University of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 5706, USA

FEATURES

source

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VERSION AF026949.1 GI:2583089
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2073)
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
TITLE Putative histone deacetylase HDAC1 from Drosophila melanogaster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2073)
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1997) Anatomy, Univ. of Birmingham, Birmingham
B15 2TT, U.K.
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Matches 727; Conservative 0; Mismatches 399; Indels 9; Gaps 2;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:17:23 ; Search time 125.93 Seconds
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12254.311 Million cell updates/sec

Title: US-09-645-337-3

Perfect score: 1800

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Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	614	34.1	1826	20	AA90837
5	549.6	30.5	1943	20	AA90840
6	530.2	29.5	2019	20	AA90839
7	523.4	29.1	1807	22	AAF80350
8	518.8	28.8	1990	21	AAZ58259
9	497.2	27.6	1805	21	AAZ58260
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12	444.6	24.7	1985	22	AAC89555	Human histone deac
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20	196.8	10.9	1654	21	AAZ93329	Human histone deac
21	196.8	10.9	2046	22	AA159530	Human polynucleoti
22	195.2	10.8	1682	22	AAH25122	Nucleotide sequenc
23	152.8	8.5	379	18	AAT86372	Partial cDNA encod
24	140	7.8	375	18	AAT86373	Human polynucleoti
25	136.6	7.6	1539	22	AA161316	Fusarium venenatum
26	134	7.4	570	21	AAF07540	Human breast tumou
27	129.2	7.2	402	22	AAH55632	Wheat histone deac
28	119.6	6.6	541	21	AAZ58261	Human ovarian can
29	109.4	6.1	222	22	AAC89707	Wild-type histone
30	98.8	5.5	1127	22	AAS00337	Cys75Ser/Cys77Ser
31	98.8	5.5	1127	22	AAS00338	Tyr297Phe mutant o
32	98.8	5.5	1127	22	AAS00339	Partial cDNA encod
33	86.2	4.8	227	18	AAT86374	Novel human polynu
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36	79.6	4.4	241	22	AAFI7915	Human colon cancer
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38	78.4	4.4	824	20	AA937387	Human secreted pro
39	78.4	4.4	1088	22	AAI13354	Human secreted pro
40	77.6	4.3	744	21	AAC95537	Human pancreatic c
41	77.4	4.3	1837	21	AAC98918	Human secreted pro
42	77.4	4.3	2864	22	AAI05415	Human secreted pro
43	77	4.3	675	22	AAI05333	Human pancreatic c
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ALIGNMENTS

RESULT 1

AAF80351
ID AAF80351 standard; DNA: 1800 BP.

XX AAF80351;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of a histone deacetylase designated ATRPD3B.
XX Histone deacetylase; ATRPD3B; gene expression; transgenic plant;
XX HDAl; ethylene-responsive phenotype; hypocotyl elongation; ds.
XX Arabidopsis thaliana.

XX Key Location/Qualifiers

XX CDS 121..1536

XX /*tag= a

XX /product= "histone deacetylase ATRPD3B"

XX CA2316036-Al.

XX 27-FEB-2001.

XX 24-AUG-2000; 2000CA-2316036.

XX 27-AUG-1999; 99US-0383971.

XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.

XX Miki B, Brown D, Tian L, Wu K;

XX WPI; 2001-258457/27.

XX P-PSDB; AAB67812.

XX

PT Methods for regulating gene expression in transgenic plants, e.g.

PT repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase

PT

PT

XX

Claim 9; Fig 1B; 9lpp; English.

PS

XX

The present sequence encodes an Arabidopsis thaliana histone deacetylase designated ATRPD3B. The protein is homologous to yeast RPD3 and HDAC1.

CC The polynucleotide sequence is used in the method of the invention.

CC The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing

CC chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence

CC encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant,

CC particularly for repressing ethylene-responsive phenotypes

CC (e.g. inhibition of hypocotyl elongation). The method is also useful

CC as a functional test for identifying a phenotype associated with

CC perturbing a gene. The histone deacetylase genes are useful for

CC altering the development of an organism.

XX

SQ

Sequence 1800 BP; 478 A; 390 C; 456 G; 476 T; 0 other;

Query Match

Best Local Similarity 99.9%; Score 1799; DB 22; Length 1800;

Matches 1799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

0;

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QY 61 taaacttggaatagagagagactctgagtgaagagagatctgagtgaagagcgag 120

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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; genetic mapping; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX KW
OS Arabidopsis thaliana.
XX PN
PN EP1033405-A2.
XX XX
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XX XX
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XX PF
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DT 13-JAN-2000 (first entry)

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Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; KW
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RNA polymerase II; transcription; plant transformation; heterochromatin; KW
disease resistance; chromatin assembly; gene activity; toxin screening; KW
pathogenicity; disease response promoter; ds. KW

AA Zea mays.

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PN WO9951731-A2.

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DR P-PSDB; AAY28797.

PT New deacetylase genes, used for producing transgenic plants which have increased disease resistance -

PS Claim 1: Page 46-49; 87pp; English.

xx CC The present sequence encodes a maize histone deacetylase. This DNA
CC belongs to family 1, 2mHD1 and appears to be regulator of promoters for
CC RNA polymerase II, for transcription of genes. The nucleotide sequence
CC can be used to transform plants and increase disease resistance by
CC altering the levels of heterochromatin, altering chromatin assembly, and
CC gene activity of the transformed plants. Additionally, compositions find
CC use in screening for toxins that affect pathogenicity and in determining
CC which disease response promoters are regulated by histone deacetylase.

Sequence 1826 BP; 437 A; 471 C; 475 G; 443 T; 0 other;

Query Match	34.1%	Score 614;	DB 20;	Length 1826;
Best Local Similarity	69.4%	Pred. No. 3e-161;		
Matches 852; Conservative	0;	Mismatches 370;	Indels 6	

Oy 145 tctctgccctcgggaccccgacgacgttaagcggcgaqtcaqtctacttctacgaqccgaq 204

Db 62 t t c c g g a a c c a a a a a a t t c c g c a c c c c c c c g c t c a g c t a t t t c t a c g a g c c g t c g 121

[illegible]

[illegible]

DB 182 caccctcgtgggtccacacagcccacagccccccacccc 241

Qy 325 gctgacgcctccgatatcgcccgattccattcgcgggagtatgttgacttctctcgtcc 384

Db 242 ggcctctgaggccgacatccgcgcgttccactccgacgactacgtcgcttccctcgctcc 301

Qy 385 gtttcgccggaatctatggcgcatccttcgcgtgcacgaaacctaaaggcattcaatgtc 444

Db 302 gccacggaaacc-----gggtgtctcgacccgcgcattaaagccttaacgtc 355

Qy 445 ggtgaggattgtcctgtcttcgacggactttttgatttttgcggtgcttcgcggagggt 504

Db 356 agtgaagactgccccgatattcgacgatatctccccctctcgcaagacctcgagctggggg 415

[illegible]

.....

[illegible]

DB 476 ggcggccctccaccacgcccaggaaggcgggttctctactatcgtaacgacalc 335

```
QY 685 gtccacatgagatagatgaggaagagcggttttacaccactgatatagattgactgtt 744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 gtccacatgagatgagatgaggaagagcggttttacaccactgatatagattgactgtt 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 745 tcttcacacaaattgggagactttttccagaaactggtcacataagagatattggcgct 804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 tcttcacacaaattgggagactttttccagaaactggtcacataagagatattggcgct 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 805 gaaagagggaataactatctctaaatttccactaaacgagtggtgatgacgatgaaagt 864
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 gccgaaggaagcattatctctgaatttcccttgagtgatggtgatgacacacc 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 865 ttcgcagacttggtagactttatccagaaggtttatggaagtgtatcagccagggca 924
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 tttcgtgctgttcaatgcatcattaaagaagtattgaggtttatcagccagagctg 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 925 gtgtttctcagtggtgctgactcttcaagttaagtgtgagtgatcggttgggtgttcaacta 984
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 gtgtttctcagtggtgctgactcttcaagttaagtgtgagtgatcggttgggtgttcaactg 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 985 tcaagtaagggtcaagctgattgcttccgtttcttaagatttcaacggttctctcatg 1044
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 tctgtgaagggtcattgctgactgcttccgtttcttaagatttcaacggttctctcatg 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1045 gtgtgggtggtgaagggttatactattcgaaattgttgcctgtgtgtgtttatgagact 1104
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Db 956 gtgttgggtggtgaagggttatactattcgaaattgttgcctgtgtgtgtttatgagact 1015
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QY 1105 gcagttgctgttggagtagagcggagcaacaaactcccttacaatgattttgagtat 1164
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Db 1016 gcagttgctgttggagtagagcggagcaacaaactcccttacaatgattttgagtat 1075
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QY 1165 ttcgcccagattatacgtcttcatgtcgaccacaaactcccttacaatgattttgagtat 1224
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Db 1076 tttggccctgattatacttctcatatccacaaactcccttacaatgattttgagtat 1135
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QY 1225 aaagatatgagagataggaacacgctgtgtggaacactttcgggactaaalacacga 1284
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Db 1136 aaggacttggagacataaagaacatgatttggagaacctgtcgaagatagaacatgtt 1195
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QY 1285 cctagcttccagttcagcacacacacacacacacacacacacacacacacacacacac 1372
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Db 1196 cccagcactcaattccatgacagacacacacacacacacacacacacacacacacacac 1255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1345 gacatggagacaaagacaaacacacacacacacacacacacacacacacacacacac 1372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1256 gacatggagacaaagacaaacacacacacacacacacacacacacacacacacacac 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5

AAx90840

ID AAX90840 standard; DNA: 1943 BP.

XX AC

XX AAX90840;

XX

DT 13-JAN-2000 (first entry)

XX

DE Maize histone deacetylase-4 DNA.

XX

KW Maize histone deacetylase; family 1, ZmHDL; promoter regulator; promoter:
RNA polymerase II; transcription; plant transformation; heterochromatin;
disease resistance; chromatin assembly; gene activity; toxin screening;
pathogenicity; disease response promoter; ds.

XX

OS Zea mays.

XX

XX Key

XX Location/Qualifiers

XX 51..1610

XX /tag= a

XX /product= "Maize histone deacetylase"

XX

XX W09951731-A2.

XX

PD

XX

PF

XX

PR

XX

XX

PA

XX

PI

XX

XX

DR

XX

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Query Match

Best Local Similarity

Matches

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

Db

14-OCT-1999.

02-APR-1999; 99WO-US07370.

03-APR-1998; 98US-0080563.

(PION-) PIONEER HI-BRED INT INC.

Baldwin DA, Briggs SP, Crane VC;

WPI: 1999-611038/52.

P-PSDB: MAY28800.

New deacetylase genes, used for producing transgenic plants which have

increased disease resistance

Claim 1; Page 60-63; 87pp; English.

The present sequence encodes a maize histone deacetylase. This DNA

belongs to family 1, ZmHDL and appears to be regulator of promoters for

RNA polymerase II, for transcription of genes. The nucleotide sequence

can be used to transform plants and increase disease resistance by

altering the levels of heterochromatin, altering chromatin assembly, and

gene activity of the transformed plants. Additionally, compositions find

use in screening for toxins that affect pathogenicity and in determining

which disease response promoters are regulated by histone deacetylase.

Sequence 1943 BP; 510 A; 498 C; 497 G; 438 T; 0 other;

Query Match

Best Local Similarity

Matches

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

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QY

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QY

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QY

Db

Db 730 ggctttttatccacagaccgggtgatgacagctcattccacaagatttgagattatt 789
 QY 771 ccagagaactgctacataagagatgttgccgctgaaaggggaaataactatgctctaaa 830
 Db 790 cctgggacagggcattcgatgtgtggcactcaagggttaataattactcctcga 849
 QY 831 ttttccactaaacagatgatgacagatgaaagtttccgagctgtgttagacctcttat 890
 Db 850 ttttccctggcagatgattgatgatgagctaccagtcgtgttccaagccaataat 909
 QY 891 ccagaaggttatggaagtgtatcaagccagagcgagctgtttcttcagttggtgctgactc 950
 Db 910 gggcaaggtgatggaggtctcaaccctgtggcagtcgtctccagtggtggtggattc 969
 QY 951 cttaagtggtgatcgttggtgtgttctcaacttatcaaggggtcacgctgattgctt 1010
 Db 970 attgtcgggtgacaggttggtgtttcaacctctctattaaaggtcacgcagaatgtgt 1029
 QY 1011 tgggttcttaagatcttcaacgcttccctcatatggtgttggtggtggtgaaggttatactat 1070
 Db 1030 aagatttatagggtcttcaacgctcccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1089
 QY 1071 tggaaatgtcccggt 1130
 Db 1090 aagaaacgttgacggt 1149
 QY 1131 caacaaactccttcaaatgagttatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1190
 Db 1150 tgacaagatgcacactaatgagttatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1209
 QY 1191 cgacccaaactctatgagatttaaacacacgcccacaaagatatgagaggataaagaacac 1250
 Db 1210 cgtcccaagtaacatggagataaaacacacacgacgacacaaattggatgacataaaacaa 1269
 QY 1251 gttgtggaaacacttctggactaatcaacgacacacacgacacacacacacacacacacac 1310
 Db 1270 acttctagataatcttcaaaactccgacatgctcctcagttcagtttcaagagcgacc 1329
 QY 1311 accag 1315
 Db 1330 tctctg 1334

RESULT 7

AAF80350

AAF80350 standard; DNA; 1807 BP.

AC AAF80350;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of a histone deacetylase designated ATRPD3A.

XX Histone deacetylase; ATRPD3A; RPD3; gene expression: transgenic plant;

XX HDAL; ethylene-responsive phenotype; hypocotyl elongation; ds.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

XX CDS 142..1647

XX /*tag= a

XX /product= "histone deacetylase ATRPD3A"

XX CA2316036-A1.

XX 27-FEB-2001.

XX 24-AUG-2000; 2000CA-2316036.

XX 27-AUG-1999; 99US-0383971.

XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.

XX MIKI B, Brown D, Tian L, Wu K;

XX WPI: 2001-258457/27.

XX P-PSDB; AAB67811.

XX Methods for regulating gene expression in transgenic plants, e.g.
 PT repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl
 PT elongation), comprises introducing genes encoding histone deacetylase
 PT .

XX Claim 9: Fig 1A; 91pp; English.

XX The present sequence encodes an Arabidopsis thaliana histone deacetylase
 CC designated ATRPD3A. The protein is homologous to yeast RPD3 and HDAL.
 CC The polynucleotide sequence is used in the method of the invention.
 CC The specification describes a method for regulating gene expression in
 CC transgenic plants. The method comprises modifying histones by introducing
 CC chimeric nucleotide sequences which have regulatory elements in operative
 CC association with a gene of interest or with a nucleotide sequence
 CC encoding histone deacetylase. The method is useful for regulating the
 CC developmental, physiological or biochemical pathway within a plant,
 CC particularly for repressing ethylene-responsive phenotypes
 CC (e.g. inhibition of hypocotyl elongation). The method is also useful
 CC as a functional test for identifying a phenotype associated with
 CC perturbing a gene. The histone deacetylase genes are useful for
 CC altering the development of an organism.

XX Sequence 1807 BP; 472 A; 386 C; 464 G; 485 T; 0 other;

Query Match

Best Local Similarity 29.1%; Score 523.4; DB 22; Length 1807;

Matches 777; Conservative 0; Mismatches 396; Indels 6; Gaps 1;

QY 137 ggggcatctctctgctgggagccgacgagcgttaagcggcgagtcagttacttctacg 196
 Db 152 ggggcaattcgtggcgtcgccgacctgatgtgtgagaggaaagtgtgtttctatg 211
 QY 197 agccgcagatcggagactactactacggttcaagccacccgagtcagtcacccgac 256
 Db 212 acctgaggtcggaattactactatgccaaggttcacccatggaagcccatcgacac 271
 QY 257 gtaggtcctatagcctaatactactatcactcaccgctcgcttagaatacagtcgc 316
 Db 272 gcatgacccatgccctcctcgtcactacggtctccttcagcatatgcaggttctcaagc 331
 QY 317 ctgagctcgtcagcctccgcatatcgccgattcctcattccgagcagatgtgtgactcc 376
 Db 332 cttcctcctccgcgcaacgtgatctcgtccttcacacgacgactgtctcttttc 391
 QY 377 tggcttccggttctcgcgggaattctatggcgatccttccgctgcacgaaacctaaagcgat 436
 Db 392 tcgcgagcattaccctgaaacccagcaagatc-----agattcgcaacttaagcgt 445
 QY 437 tcaatgctggtaggattcctgtcttcgacggacatttttatttttgcgtgtcttcg 496
 Db 446 tcaatgttgtagagactgctcgtctttgacggcgttttattccttttgcagactatg 505
 QY 497 ccggaggttctattgggtcgtccgtcaaatataacagacagacgctgatatcgctatca 556
 Db 506 ctggaggtatctgtgtgtgctgtcgaacttaacacggcctctgcgattatgcacatca 565
 QY 557 attggggcgttggtctcaccatgctaaagaaagcaggtcttctggttttctatgtaa 616
 Db 566 actgggctggtgtgtctccatcagcgttaagagtgcgagcctctgcttctgttactca 625
 QY 617 acgacatcgtgctagggattctggagttgctcaagatgtttaagcgggtctctacatag 676
 Db 626 atgatcgtcttagctatcctcagagctccttaacagcatgagcgtgtctttatgctc 685
 QY 677 atattgatgtccaccatgagatggagtggaagagcgtttttacaccactgatagatta 736
 Db 736

Db 474 gcagatgcataatttaattgttgagagattgtccagcgtttgatggacttttgatt 533
 Qy 483 ttgcggtgctccgagaggttctattgtgctgcgtccaaattaaacagacagcgc 542
 Db 534 ttgcaactcctaactggcgttcagttgctgagcgtgaagttaaaccgcaacagac 593
 Qy 543 tgatagctcaatggcgtggcgttcaccatgctaaagaaagcagcgtctctgg 602
 Db 594 tgatagcgttaattggcgtgaggttacatcatgctaaagaaatcacgaatcagc 653
 Qy 603 gtttgctgtataaacacacatgctgtagggattctgagttcctcaagatgtttaagcg 662
 Db 654 attctgttaactgaatgattgtgttgcctccttggaattactaaatgatcatcag 713
 Qy 663 gtttctctacatagattgatgtccaccatggagatggagtggaagaacggtttacac 722
 Db 714 agtcttatattgaatagataatcatctcatgtggtgtggaagaagctttttatcac 773
 Qy 723 cactgtagaggttatgactttcttcccaaaatttggggacttttcccgagaaactgg 782
 Db 774 aacagatcgtgtaatgacgttatccatccataaataatggggaatacttctcggcacag 833
 Qy 783 tcacataagagatttggcgtcaaaaagggaaaataactatgctctaaatttccactaaa 842
 Db 834 agactgagggatattgtgtcgtgaaaagcaaaactatgctgtcaattttccaatgtg 893
 Qy 843 cgtatgtatgacatgaagatttccgcagcttgttttagacctcttatccagaaggttat 902
 Db 894 tgatggtatagatgagtcataatggcgagatatttaagcctattatctcaagaaggat 953
 Qy 903 ggaagtgatatacagcagagcaggtttcttcagtggtgtgctgactccttaagtgtga 962
 Db 954 ggagatgtatacaactagtgctgtgtattacagtggtgcagactcattatctgtga 1013
 Qy 963 tcggttggtgttgcacttatcagtcaggggtcagcgtgattgcttcgtttcttaag 1022
 Db 1014 tagactgggtgttctcaatcaacagtcacagtcaggtcatgctaaatgtgagaagtgtaaa 1073
 Qy 1023 atcttaacacgttctctcatggtgttgggtgtggaaggtatactattcgaagtgtgc 1082
 Db 1074 aacttttaacttaccattactgattggtgagaggtgtgtacacacatcgtaatgtgc 1133
 Qy 1083 ccgtgtggtgttatgagacgtgattgtgttggagtagagcggacacacaaactccc 1142
 Db 1134 tcgattgtggacatgagacgtcagttgctcctgtgtgtgagattcccaatgagttgcc 1193
 Qy 1143 ttacaatgagttattttagtatttccgcccagattatacgttctcatcgaaccaatgcc 1202
 Db 1194 atataagattacttttagtattttggaccagacttcaaacgtgcataattagttctcaa 1253
 Qy 1203 tatggagaatttaacacgcgcacaaagatatggagagataaggaacacgtgtgtggaaca 1262
 Db 1254 catgacaaccagaaactcagaatataatggaaaagataaaacagcgtttgttgaaa 1313
 Qy 1263 actttcgggactataacacgcacactagctccagtttcagtcacacacacacag 1315
 Db 1314 ttgcgcagtttacctatgcactgtgttccagatgcaagctattccagaag 1366

RESULT 12

AAC89555

ID AAC89555 standard; DNA: 1985 BP.

XX XX

AC AAC89555;

XX XX

08-MAR-2001 (first entry)

XX XX

Human histone deacetylase HDAC-2 coding sequence.

XX XX

Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

KW gene therapy; ds.

XX XX

OS Homo sapiens.
 XX WO200071703-A2.
 PN 30-NOV-2000.
 PD 03-MAY-2000; 2000WO-1B01252.
 PF 03-MAY-1999; 99US-0132287.
 PR (METH-) METHYLOGENE INC.
 PA Macleod AR, Li Z, Besterman JM;
 PI WPI: 2001-016407/02.
 XX P-PSDB; AAB49955.
 DR Antisense oligonucleotide that inhibits expression of a histone
 XX deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal -
 PS Disclosure; Page 53; 125pp; English.
 XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia.
 XX Sequence 1985 BP; 626 A; 360 C; 454 G; 545 T; 0 other;

Query Match 24.7%; Score 444.6; DB 22; Length 1985;
 Best Local Similarity 61.4%; Pred. No. 6.2e-114;
 Matches 733; Conservative 0; Mismatches 454; Indels 6; Gaps 1;

QY 123 ggagggcagacgaagcggcatctctgcgtcgggacccgacggcgttaagcggcag 182
 Db 180 ggtggcggcgttggcgggagccatggtgacagtcgaagggcgcaaaaaaagt 239
 QY 183 cagtactctcagacccagcagatcggagactactactactacggtcaaggccacccgatga 242
 Db 240 ctgctactacacgggtgatttgaaattattattgacaggggtccatcccatga 299
 QY 243 gctccacggatcgtatgctcatgactgaactaatcattcactatcacctcacgcgtc 302
 Db 300 gctcatagaatccgatgaccataacttgcgttaaatcttggttattacacagaaat 359
 QY 303 agaaatcagtcgcctagcctgcgtcagcgtccgatatcggcgttccttcgcgga 362
 Db 360 ggaatatatagcccaataaagccactgccgaagaaatgacaaaatatcacagtgatga 419
 QY 363 gtagttgacttctcgttccgttttcgcgggaattctatggtggtccttcctcgcgcag 422
 Db 420 gtatatcaaatcttcacgttcaataagaccagcataacatg-----tctgagtagtaa 473
 QY 423 aaacctaaagcgttccaatgcgtggtgaggttctctgtcttccttcgcaggtttttgatt 482
 Db 474 gcagatgcataatttaattgttgagaagattgtccagcgtttgatggacttttgatt 533
 QY 483 ttgcgtgttccgcggaggttctattgtgtgcgtcctcaaatgaaacagacagcgc 542
 Db 534 ttgcagctcctcaactggcgttccagttggtgagcgttgaaatgaaacagacagac 593
 QY 543 tgatagcgtatcaattggggcgtgtggttccaccatgctaaagaaagcaggtctctgg 602
 Db 594 tgatagcgttgaattggcgtgaggtattacatcatgctaaagaaatcacgaatcagc 653
 QY 603 gtttgcgtgtataacacacatcgtgtagggattctggtgaggtgtcctcaagatgtttaagcg 662
 Db 654 attctgttaactgaatgattgtgctgccatccttgatgactactaagaatcatcagcag 713

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QY 663 gggtctctacatagatgatggtccaccatggagagtgagtggaagaagcgtttttacac 722
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QY 723 cactgtagatgattgactgcttctccacaaatttgggacttttcccaaggaactg 782
Db 774 aacagatcgtgtaagacggtatcatctccataaataagggaatacttctccctggcacagg 833
QY 783 tcacataagagattgttggcgtgaaaggaaataactatgctctaaatgttccactaaa 842
Db 834 agacttggggatattgttgcgtgaaaggaaataactatgctctcaatttcccaatgtg 893
QY 843 cpatggtatggacgatgaagtttccgcagctgtttagacactcttaccagaaggttat 902
Db 894 tgatgtagatgtagtgcattatggcgagatatttaagctattatctcaaaaggtgat 953
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QY 963 tcggttgggtggttcttcaactatcagtcgaaggtggtggtggtggtggtggtggtggt 1022
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Db 1134 tcgagtgtgacatagactgagtgctgtggtggtggtggtggtggtggtggtggtggt 1193
QY 1143 ttacatagagtatttggatttccgcccagattatcagcttcatgctgaccccaagtc 1202
Db 1194 atataatgattacttggatttggaccagacttcaaacgtcattatgctcctcaaa 1253
QY 1203 tatggagaatttaaacacgcccacagatagtgagaggtggtggtggtggtggtggtg 1262
Db 1254 catgacaaacaggaacactccagataatagtggtggtggtggtggtggtggtggtg 1313
QY 1263 acttctgggactaatacacgacactagcgtcagtttccagcacacacacacag 1315
Db 1314 ttggcagtgtaactcatgacactggtgtccagatgcaagctatttccagaag 1366

RESULT 13
AAX90838
ID AAX90838 standard; DNA; 1475 BP.
AC AAX90838;
XX
XX
DE 13-JAN-2000 (first entry)
XX
XX
DE Maize histone deacetylase-2 DNA.
XX
XX
KW Maize histone deacetylase; family 1, ZmHDL1; promoter regulator; promoter;
KW RNA polymerase II; transcription; plant transformation; heterochromatin;
KW disease resistance; chromatin assembly; gene activity; toxin screening;
KW pathogenicity; disease response promoter; ds.
XX
XX
OS Zea mays.
XX
XX
FH Key Location/Qualifiers
FT CDS 29..1084
FT /*tag= a
FT /product= "Maize histone deacetylase"
XX
XX
W09951731-A2.
XX
XX
PD 14-OCT-1999.
XX
XX
PF 02-APR-1999; 99WO-US07370.
XX
XX

```

```

PR 03-APR-1998; 980S-0080563.
XX
XX PA (PION-) PIONEER HI-BRED INT INC.
XX
XX PI Baldwin DA, Briggs SP, Crane VC;
XX
XX WPI: 1999-611038/52.
DR P-PSDB; AAY28798.
XX
XX New deacetylase genes, used for producing transgenic plants which have
XX increased disease resistance
XX
XX Claim 1; Page 51-53; 87pp; English.
XX
XX The present sequence encodes a maize histone deacetylase. This DNA
XX belongs to family 1, ZmHDL1 and appears to be regulator of promoters for
XX RNA polymerase II, for transcription of genes. The nucleotide sequence
XX can be used to transform plants and increase disease resistance by
XX altering the levels of heterochromatin, altering chromatin assembly, and
XX gene activity of the transformed plants. Additionally, compositions find
XX use in screening for toxins that affect pathogenicity and in determining
XX which disease response promoters are regulated by histone deacetylase.
XX
XX Sequence 1475 BP; 388 A; 342 C; 376 G; 369 T; 0 other;

```

```

Query Match 24.5%; Score 441.4; DB 20; Length 1475;
Best Local Similarity 71.9%; Pred. No. 4.2e-113;
Matches 577; Conservative 0; Mismatches 226; Indels 0; Gaps 0:
QY 570 gttccaccatgtaagaaagcgaggtcttgggttttggctatgttaacgacatcgtgct 629
Db 160 gccccacacgccaagaagcgaggtcctcggtctgtctacgtcaacgacatcgtcct 219
QY 630 agggattcggagtggttccaagatgtttaagcgggttctctacatagatattgatgcca 689
Db 220 cgcctctcctgagctcctcaagttccacagcgtgtgctatattgacatattgatgcca 279
QY 690 ccatggagatggatgggaagcggtttacaccactgataagttatgactgttctctt 749
Db 280 ccatggagatgggtggagagggccttctcaacacaaacgacatcgtactgttctctt 339
QY 750 ccacaaatttgggagacttttccaggaaactggtccacataagatgttggcgtgaaaa 809
Db 340 tcacaaagtatgggatttttccctggtactggacatatacactgactgactggtggcagcga 399
QY 810 aggaataactatgctctaaatgttccactaaacgagtggtgacatgaaagtcttcg 869
Db 400 aggaagcattatgctctgaatgttccctgagtggtggtggtgacacacacctctcg 459
QY 870 cagctgtttagacctcttaccagaggtttatggaagtgtatcagccagagggcagttgt 929
Db 460 tggctgttccaatgcatcattaaagaagtattatggaggtttatcagccagcgtggtgtg 519
QY 930 tctcagtggtggtgactccttaagtgtggtggtggtggtggtggtggtggtggtggtg 989
Db 520 cctcaatggagtgactccttctggtggagacaggttaggtggttctcaactgctgct 579
QY 990 caaggttcaactgactgcttctggttcttaagatcttcaaacgttctctcactggtggt 1049
Db 580 gaaggttcaactgactgcttctggttcttaagatcttcaaacgttctctcactggtggt 639
QY 1050 ggggttgaaggttatactatgaaatgttggcctgttgggtgttattgagactgcaqt 1109
Db 640 aggttgggtgaggtttacacatcagaaatgttgcagctgctggtggtacgagacgcaql 699
QY 1110 tgcgttggagtagagcggacacaaactccttacaatgagttattttagtatttcygg 1169
Db 700 tgcgttggagtagagcggacacaaactccttacaatgagttattttagtatttcygg 759
QY 1170 cccagattatacgtcttcatgtccgaccccaagtcctatgagaaatttaacaccccaaga 1229
Db 760 ccttgattatacgtcttcatgtccgaccccaagtcctatgagaaatttaacaccccaaga 819

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QY 1134 caaacctccctaccatagatatttgatgtatttgcggccagattatacagcttcattgtcga 1193
 Db 978 tgagctccatataatgactactttgaatactttgaccagatttcaagctccacatcag 1037
 QY 1194 ccaagctcatgaggaatttaaacacgcccgaagatatggagagataaggaacacglt 1253
 Db 1038 tectccaatagactaacgaacacgaatgagtacctggagaagatacaaacagcgaact 1097
 QY 1254 gctgggaacacttcgggagctatacacgcacactagcgtccagtttcag 1302
 Db 1098 gtttgagaaccttagaactcgtccgcacgcacactgggtccaaatgcag 1146

RESULT 15

AAC89554

ID AAC89554 standard; DNA; 1611 BP.

AC AAC89554;

XX 08-MAR-2001 (first entry)

XX Human histone deacetylase HDAC-1 coding sequence.

XX Histone deacetylase: HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; ds.

XX Homo sapiens.

XX WO200071703-A2.

XX 30-NOV-2000.

XX 03-MAY-2000; 2000WO-IB01252.

XX 03-MAY-1999; 99US-0132287.

XX (METH-) METHYLOGENE INC.

XX Macleod AR, Li Z, Besterman JM;

XX WPI: 2001-016407/02.

XX P-PSDB; AAB49954.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal -
 PS Disclosure; Page 50-51; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia.

XX Sequence 1611 BP; 428 A; 385 C; 440 G; 358 T; 0 other;

Query Match 24.3%; Score 436.6; DB 22; Length 1611;
 Best Local Similarity 62.4%; Pred. No. 9.6e-112;
 Matches 704; Conservative 0; Mismatches 419; Indels 6; Gaps 1;

QY 174 gcggcgagtcagttactctacagccgacgactcagactactactacggtcaaggcca 233

Db 134 gaggaaagctgttactactacgaggggaggttggaataactattatggaaaggcca 193

QY 234 ccgagtaagcctaccggagtcggtatggtcctatagcctaatcattcactacactcca 293

Db 194 cccaatgaagcctccaggaatccgcatgactcataattgtcgtcaactatggtctcta 253

QY 294 ccgtcgcttagaaatcagtcgacctagctcgctgacgacctccgatatcgccgattcca 353

Db 254 ccgaaaaatgaaaatctatcgccctcacaaagccaatgctgagagatgaccaagtacca 313
 QY 354 ttccgcggagiatgttgacttccctgcgttccggttccggaatctatggcgatcctte 413
 Db 314 cagcgatgactacataaattctgctccatccgtccatatacaactgctggagtagcag 373
 QY 414 cgtgacgcaaaccttaagcgattcaatgctcggtgagagattgctcgtcttcgacgact 473
 Db 374 c-----aagcagatgcagagattcaacgttggtagagactgtccagtattcgatgcct 427
 QY 474 ttttgattttgcccgtctccgcggaggtttctatgtgtgctgcgtccaaatlaaacag 533
 Db 428 gtttgagttctgctcagttgctactggtggttctgtggaaggtgctgtgaacttaataa 487
 QY 534 acaggacgctgatactcattcaattggcggtggggttccacctgctaaagaagcga 593
 Db 488 gcagcagcggacatcgctgaaattgggtggggtggtccacctgcaagaagagtcga 547
 QY 594 ggctctgggtttgctatgtaaacgacatcgctgtagggattcttgaggtgctcaagat 653
 Db 548 ggcattcggtctgttaactcaatgatatcgcttggccatctggaactgctaaagta 607
 QY 654 gtttaagcgggttctctacatagattgattgctccacctgagatggagtggaagcga 713
 Db 608 tcaccagagggtgctgtacattgacattgattcaccattgacggcgtggaagagcgc 667
 QY 714 gttttacaccatgataagattatgactgtttcttccacaaatttgggactttttccc 773
 Db 668 cttctacaccggagccgggtcactgactgtctcttcaagattgagagtagtctccc 727
 QY 774 aggaactggtcacataagagattgttgcgctgaaaggggaaataactatgctctaaatgt 833
 Db 728 aggaactgggacctacgggatatcggggtggcaaggcaagattatgctgttaacta 787
 QY 834 tccactaaacgatggatggacgatgaaagtttccgcagctgtgttagaacctcttatcca 893
 Db 788 ccgcctcagacgggattgtagcagactcctatgagggccattttcaagcggctcatgtc 847
 QY 894 gaaggttatggaagtgtatcagccagagagcaggtgtcttcagttggtgctgactcctt 953
 Db 848 caaagtaalgagatgttccagcctagtcggtggtgttaccagtgtggtcagactccct 907
 QY 954 aagtggtgatcgggttggttcttcaactatcagtcacgaggggtcagcgtgattgcttcg 1013
 Db 908 atctggggatcggttaggtgttctcaactataactataaaggacacgccaagtgtgtga 967
 QY 1014 gttcttaagatcttacaacgcttccctcactggtgtggtggtggaaggtatactattcg 1073
 Db 968 atgtgcaagagctttaacctgctatgctgtagtggtggagcgggtgttaccaccttcg 1027
 QY 1074 aaatgttcccggttctggtgttatgagactgcagttgctgttgagtagagccggacaa 1133
 Db 1028 taacgtttcccggtgctggacatatgagacagctgtgcccctgtagacggagatccctaa 1087
 QY 1134 caaacctcccttacaatgagatttttgatttccggcccaagattatcagcttcatgtcga 1193
 Db 1088 tgagcttccatacaatgactactttgaatactttggaccagatttcaagctccacatcag 1147
 QY 1194 cccaagctcctatggagaatttaaacacgcccgaagatatgagagggataagaacacgtt 1253
 Db 1148 tcttccaatagtaataaccagaacacgaatgagtactcgtggagagatcaaacagcagct 1207
 QY 1254 gctggaaacaacttctgggacttaatacacgcacactagcgtccagtttcag 1302
 Db 1208 gtttgagaaccttagaatgctgcccgcagcagccttggggtcccaaatgcag 1256

Search completed: March 8, 2002, 23:41:43
 Job time: 1460 sec

Db 1330 tcctq 1334

RESULT

US-09-282-305-3

: Sequence 3, Application US/09282305

; Patent No. 6287843

GENERAL INFORMATION:

APPLICANT: Baldwin, Donald A.

APPLICANT: Briggs, Steven P.

APPLICANT: Crane, Virginia C.

TITLE OF INVENTION: Maltze Histone Deacetylases And Their Uses

; FILE OF INVENTION: FILE
; FILE REFERENCE: 5718-44.; FILE REFERENCE: 3718 44;
; CURRENT APPLICATION NUMBER: US/09/282.305

: CURRENT FILING DATE: 1999-03-31

CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080 563

; PRIOR APPLICATION NUMBER: 807
 ; PRIOR FILING DATE: 1998-04-03

, PRIOR FILING DATE: 1998-
 : NUMBER OF SEQ TO NOS. 19

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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver 3.0

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; SOFTWARE:
; SEQ ID NO 3

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; SEQ ID NO 3
: LENGTH: 1475
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LENGTH: 12
TYPE: DNA

TYPE: DNA

ORGANISM: Zea

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; FEATURE:
NAME/KEN:

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; NAME/KEY: CDS

; LOCATION: (

Query Match

Query MACCN	24.56;	Score 441.4;	DB 4;	Length 1473;
Best Local Similarity	71.98;	Pred No 1	1e-116.	

Best Local Similarity 71.9%; F1ed: NO: 1.1E-110;
Matches 577: Conservative 0: Mismatches 226:

QY	570	gcttcacatgctaaagaaagcagaggtctctgggttttgctatgataaacacatcgtcgt	629
Db	160	gccaccacgcgcgaagagcgaggtccgggtctctacgcacacatcgtcct	219
QY	630	agggattctggagttgctcaagatgtttaagcgggtctctacatagatgattgatgcc	689
Db	220	cgcacctcgcagctcccaagtccacagcggtgctatatagacattgatgcc	279
QY	690	ccatgagatgagtggaagaagcgttttacaccactgatagattatgactgtttctt	749
Db	280	ccatgagatggcgtggagagcctctctacacaaacgagctgactgttctct	339
QY	750	ccacaaatttgggacttttccaggaactggccacataaagatgttggcgtcaaaa	809
Db	340	tcacagatggggatttttccctggctacggacatacactgacgttgggcagcgca	399
QY	810	agggaaactatgctcaaatgttccactaaacgagtgtatgacgatgaagattccg	869
Db	400	agggaaacattatgctcgaatgttccctgagtgatggtatgacaccaccttcg	459
QY	870	cagctgttttagacctttatccagaaggttatggaagtgtatcagccagagcgttgt	929
Db	460	tggctgttccatgcacattaaagaagtattagaggtttatcagccagacgtgggtgt	519
QY	930	tcttcagttggtgctgactccttaagtgggtgatcgttggttggttcactatcagt	989
Db	520	cctccaatgcggagctgactcttggctggagacaggttaggttgctcaacctgctgt	579
QY	990	caagggtcacgctgatgcttcgtctcttaagatcttacaacgtctcctctcatgggtt	1049
Db	580	gaagggtcatgctgactgcctcgttctctttaggtctgtacaatatctcatgaggttt	639
QY	1050	gggtggtgaagggtatactattcgaattgttgcctgttgcgttggtttatgagactcagt	1109
Db	640	aggtggtggaggttacaccatcagaattgttgcacgtcgtgtggtgcacgagaccgagt	699
QY	1110	tgctgttgagtagagccggacacaaactccctacaatgagttatttgatatttcgg	1169
Db	700	tgcgttgagttgaaactgatacaacgtccttacaatgattactatgactgacttgg	759

[illegible]

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Db 1101 TCCTTCCAATATGACTAACCAGAACACGAATGAGTACCTGGAGAGATCAACACGCGACT 1160
Qy 1254 gctggacaacatttcgggactaatacacgcacacccagctgcagtttcag 1302
Db 1161 GTTTGAGACCTTAGAATGCTGCCGACGACCACTGGGGTCCAATGCGAG 1209

RESULT 6
US-08-717-365-2
: Sequence 2, Application US/08/717365
: Patent No. 5763182
: GENERAL INFORMATION:
: APPLICANT: NAKAMURA, YUSUKE
: APPLICANT: FURUKAWA, YOICHI
: TITLE OF INVENTION: RPDL PROTEIN AND DNA
: TITLE OF INVENTION: ENCODING THE SAME
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
: STREET: 2026 Rambling Road
: CITY: Kalamazoo
: STATE: Michigan
: COUNTRY: USA
: ZIP: 49008-1699
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT Compatible
: OPERATING SYSTEM: MS-DOS 5.0
: SOFTWARE: WordPerfect 5.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/717,365
: FILING DATE: 23-SEP-1996
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/528 255
: FILING DATE: September 14, 1995
: APPLICATION NUMBER: JP6-227876
: FILING DATE: 22-SEPTEMBER-1994
: APPLICATION NUMBER: JP7-183763
: FILING DATE: 20-JULY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Terrynence F. Chapman
: REGISTRATION NUMBER: 32549
: REFERENCE/DOCKET NUMBER: Furuya Case 1335
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (616) 381-1156
: TELEFAX: (616) 381-5465
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 211
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: IMMEDIATE SOURCE:
: LIBRARY: human fetal lung cDNA library
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 64..1512
: IDENTIFICATION METHOD: experimental examination
: US-08-717-365-2

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Query Match	24.2%	Score 435;	DB 1:	Length 2111;
Best Local Similarity	62.3%;	Pred. No. 9.2e-115;		
Matches 703; Conservative	0;	Mismatches 420;	Indels 6;	Gaps 1;
Oy	174	gcggcgagtcagtctactctacgagcgcgcgatcgaggactactactacgtcaaggcca	233	
Dd	87	gagaaagctctgtttactactacgacggggatgttggaatttactatttatggacaagggcca	146	

Db 681 aaaggaagaaatattatgtctatcaaacattccacttaaaagatgggatagatgacacta 740
Qy 863 gtttcgcagctgttttagaacctcttaccagaaggtttatgaaagtgtatcagccagagg 922
Db 741 gctttactcgccttttaaaacaaattattgccaaggttgttgagacatatcgtcgtgtg 800
Qy 923 cagttgttcttcagttggtgtgactccttaagttggtgtgagttggtgttctcaact 982
Db 801 ctattgttctcaatgtgggctgattcattgagcagggatcgttttaggtgttcaatc 860
Qy 983 tatcagtcagaggtcagctgtattcctcctgtgttcttaagatcttacaacgttctctca 1042
Db 861 tctctattgaagggcctgctgaattgttaagtttgcagaataatcaattatcccttc 920
Qy 1043 tgggtgtgggtgtaagaggtatactattcgaatgttgccgtgtgctgtgttatgaga 1102
Db 921 tggtaactgagaggtgtgatacaccacaggaagatgtgacacggtgttggcgtgtgaaa 980
Qy 1103 ctgcagttgctgttggagtagagccgggacaacaaacctcttacaatgagtattttgagt 1162
Db 981 ctgggggtccttttagacacagaaacctcccaaatgagattcccaaaaatgaatatattgagt 1040
Qy 1163 atttcggccagattatagcttctatgtcgaccccaagtcctatgagaaatttaaacacgc 1222
Db 1041 actttgtccagattatatactgaaagtcccaatttgaacatggacaaatttgaacagta 1100
Qy 1223 ccaagatatgagaggaataagaaacacagttgtgtgaaacacttccggagactaatacag 1282
Db 1101 agacctatctcgttcaatcaagtgcaagtgatggaggttgcggtacatacagagcatg 1160
Qy 1283 caactagctcagtttccagcacacacaccacagtcacatcgatttttgagcagccggag 1342
Db 1161 ctcttggttcaaatgcaagaggttctctcccgatttttatatccggagactttgatgaag 1220
Qy 1343 atgacatgga 1352
Db 1221 atgaattgga 1230

RESULT 8

US-09-998-416-317

; Sequence 317, Application US/08998416

; Patent No. 6239264

; GENERAL INFORMATION:

; APPLICANT: Philippsen, Peter

; APPLICANT: Pohlmann, Rainer

; APPLICANT: Steiner, Sabine

; APPLICANT: Mohr, Christine

; APPLICANT: Wendland, Jürgen

; APPLICANT: Knechtel, Philipp

; APPLICANT: Reibschung, Corinne

; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL

; NUMBER OF INVENTION: AND USES THEREOF

; NUMBER OF SEQUENCES: 1152

; CORRESPONDENCE ADDRESS:

; ADDRESS: No. 6239264artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 6239264th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/998,416

; FILING DATE: 24-DEC-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: CH 0016/97

; FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 317:
SEQUENCE CHARACTERISTICS:
LENGTH: 841 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE: PAG1256UP
ORGANISM: US-08-998-416-317

Query Match 10.2%; Score 184; DB 4; Length 841;
Best Local Similarity 60.6%; Pred. No. 3.8e-43;
Matches 337; Conservative 0; Mismatches 215; Indels 4; Gaps 2;

Qy 553 atcaattggggcgggtgggtcttcacatgctaaagaaagcagaggtctctgggtttgttat 612
Db 2 ATCAACTGCTCGGCGGGCTGCACCCAGCAAGAGCAATCTCTCGGCTTCTGTTTAC 61
Qy 613 gtaaacacatcgtcgttagggattctgagttgctcaagatgtttaacgggttctctac 672
Db 62 GTGAACGACATTTGTTGGCGCTTGAATCTGCTGCCTACCAACCCACGCGTTCGTGAC 121
Qy 673 atagatatgtatccaccatggagatggagtgaaagcgttttacacacacagtaga 732
Db 122 ATTGACATTGATCGCACCGGACGGGTGTCCAAAGAACGATCTTACACTACTGACCGC 181
Qy 733 gttatgactgtttcttcacaaat---ttgggactttttccacaggaaactgggtcacata 789
Db 182 GTGTTTCACGGTCTCGTTCACAAAGTACAATGCTGAGTTTTTTCGGGGAACGGGGATTG 241
Qy 790 agagatgttgcgctgaaaaaggggaaataactatctctaaatgttccactaaacagatgt 849
Db 242 GATGATCGGATGCTCGCGCGCAAGCACTTTTCGCTGAATGTGCGCTCAATGACCGC 301
Qy 850 atgacgatgaaagtcttcgcagctgttttagacctctatccagaaaggttatggaagt 909
Db 302 ATCGATGATGATTCGTACATCAACTTATTAAAGACCATCATAGACCCCTAGTACATCA 361
Qy 910 tatcagccagagggcagttgttctcagttggtgtgactccttaagtggtgattggtt 969
Db 362 TACAAGCCACACAGTAATTATTACGAATGTGGAGCAGACTCTTTGGGGCATGACAGACTG 421
Qy 970 gtttgcctcaacttatcagtcaggtcaaggtcagctgattccttcggttcttaagatctt 1029
Db 422 GGGTGTTCATTAATCTAAATATCAGAGCCCGGCGGAGTCCGTCATTTGTGAAG-TCGTT 480
Qy 1030 aacgttctctcaggtgttgggtgaaaggtatattcagaaatgttgcggttgc 1089
Db 481 GGGATACCTATGCTATGCTGCTGGTGGAGGTGTACACCCCGAGGAATGTGTGCGGGCTA 540
Qy 1090 tgggttatgagagctg 1105
Db 541 TGGAGTACGAGAGAG 556

RESULT 9

US-09-013-634-1

; Sequence 1, Application US/09013634

; Patent No. 5945307

; GENERAL INFORMATION:

; APPLICANT: M. Alexandra Glucksmann and Keith Robison

; TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/09/013,634
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1194
US-09-013-634-1

Query Match 4.2% Score 75; DB 2; Length 2581;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 aaaaaaaaaaaaaaaaaagggcgccgtctagaggtccaaagcttacgacgc 1785
Db 2497 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGGATCCAAAGCTTACGTACGCG 2556
QY 1786 tgcacgacgtcat 1800
Db 2557 TGCATGGGACGTCTAT 2571

RESULT 10
US-09-118-442-29/c
Sequence 29, Application US/09118442B
Patent No. 6197561
GENERAL INFORMATION:
APPLICANT: Martino-Catt, Susan J.
APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry R.
APPLICANT: Wang, Xun
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
FILE REFERENCE: 0706
CURRENT APPLICATION NUMBER: US/09/118,442B
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/055,446
EARLIER FILING DATE: 1997-08-11
EARLIER APPLICATION NUMBER: 60/055,526
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: 60/053,944
EARLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1330
TYPE: DNA
ORGANISM: Zea mays
US-09-118-442-29

Query Match 4.0% Score 72; DB 4; Length 1330;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 aaaaaaaaaaaaaaaaaagggcgccgtctagaggtccaaagcttacgacgtgc 1788
Db 94 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGGATCCAAAGCTTACGTACGCGTGC 35
QY 1789 atgcgacgtcat 1800
Db 34 ATGGCAGGTCTAT 23

RESULT 11
US-09-677-064-29/c
Sequence 29, Application US/09677064
Patent No. 6291224
GENERAL INFORMATION:
APPLICANT: Martino-Catt, Susan J.
APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry R.
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
FILE REFERENCE: 0706D
CURRENT APPLICATION NUMBER: US/09/677,064
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
PRIOR APPLICATION NUMBER: 60/055,526
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 60/053,944
PRIOR FILING DATE: 1997-07-28
PRIOR APPLICATION NUMBER: 09/118,442
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1330
TYPE: DNA
ORGANISM: Zea mays
US-09-677-064-29

Query Match 4.0% Score 72; DB 4; Length 1330;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 aaaaaaaaaaaaaaaaaagggcgccgtctagaggtccaaagcttacgacgtgc 1788
Db 94 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGGATCCAAAGCTTACGTACGCGTGC 35
QY 1789 atgcgacgtcat 1800
Db 34 ATGGCAGGTCTAT 23

RESULT 12
US-08-383-756-1
Sequence 1, Application US/08383756
Patent No. 5654495
GENERAL INFORMATION:
APPLICANT: Dehesh, Katayoon
APPLICANT: Voelker, Toni Alois
APPLICANT: Hawkins, Deborah
APPLICANT: Davies, Huw Maelor

;; TITLE OF INVENTION: MOLECULES
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: FastSeq for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/964,127
;; FILING DATE: 06-NOV-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Crews, Ph.D., L. Lee
;; REGISTRATION NUMBER: P-43,567
;; REFERENCE/DOCKET NUMBER: 07334/038001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2460 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 498....2057
US-08-964-127-1

Query Match 3.8%; Score 68; DB 4; Length 2460;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1726 aaaaaaaaaaaaaaaaaagggcgccgctctagaggatccaaagcttacgtacgcg 1785
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Db 2393 AAAAAAAAAAAAAAAAAAGGGCGCCGCTCTAGAGGATCCAAAGCTTACGTACGCG 2452
QY 1786 tgcatcg 1793
Db 2453 TGCATCG 2460

RESULT 15
US-09-118-442-31
;; Sequence 31, Application US/09118442B
;; Patent No. 6197561
;; GENERAL INFORMATION:
;; APPLICANT: Martino-Catt, Susan J.
;; APPLICANT: Wang, Hongyu
;; APPLICANT: Beach, Larry R.
;; APPLICANT: Wang, Xun
;; APPLICANT: Bowen, Benjamin A.
;; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
;; TITLE OF INVENTION: Plants and Uses Thereof
;; FILE REFERENCE: 0706
;; CURRENT APPLICATION NUMBER: US/09/118,442B
;; CURRENT FILING DATE: 1998-07-17
;; EARLIER APPLICATION NUMBER: 60/055,446
;; EARLIER FILING DATE: 1997-08-11
;; EARLIER APPLICATION NUMBER: 60/055,526
;; EARLIER FILING DATE: 1997-08-08

;; EARLIER APPLICATION NUMBER: 60/053,944
;; EARLIER FILING DATE: 1997-07-28
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 31
;; LENGTH: 1255
;; TYPE: DNA
;; ORGANISM: Zea mays
US-09-118-442-31

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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 1161 aaaaaaaaaaaaaaaaaagggcgccgctctagaggatccaaagcttacgtacgcg 1220
QY 1794 acgtcat 1800
Db 1221 acgtcat 1227
Search completed: March 8, 2002, 23:42:50
Job time: 1412 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:14:58 : Search time 1204.3 Seconds
(without alignments)
16061.116 Million cell updates/sec

Title: US-09-645-337-3

Perfect score: 1800

Sequence: 1 gtgccacacactcctagtaa.....acgcgtgcagtcgaagtcac 1800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rnd:*
20: em_gss_vrt:*
21: em_gss_other:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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3	428.8	23.8	737	11	BI177518	BI177518 EST518463
C 4	380.8	21.2	385	10	AV567115	AV567115
5	365	20.3	765	10	AJ394397	AJ394397
6	353	19.6	999	10	AL518877	AL518877
7	347.2	19.3	977	13	CNS072YS	AL426842 clone BA0
C 8	347	19.3	907	13	CNS06FTS	AL414998 T3 end of
9	343.4	19.1	609	10	AT726977	AT726977 BNGCH1702
C 10	342.2	19.0	1030	13	CNS06MLI	AL405628 T3 end of
11	341	18.9	617	11	BF324960	BF324960 su29e12.y
12	340.2	18.9	919	10	AL531607	AL531607

13	334.2	18.6	621	10	AW217600	AW217600 EST296314
14	333.6	18.5	431	10	AA394745	AA394745 26542 Lam
15	332.2	18.5	847	10	AL558916	AL558916
16	329.6	18.3	946	10	BE036122	BE036122 M007D08 M
17	325.8	18.1	640	11	BG449764	BG449764 NF007G021
18	322.6	17.9	577	11	BF176911	BF176911 EN1_4_C06
19	321	17.8	910	11	BG756668	BG756668 602715527
20	319.4	17.7	719	10	AU132519	AU132519 AU132519
C 21	318.8	17.7	881	13	CNS0744AN	AL428565 clone BA0
22	318.8	17.7	898	10	AL541430	AL541430
23	317.2	17.6	917	11	BI118849	BI118849 EST237 DI
24	316.8	17.6	819	10	BE558877	BE558877 HV_C06002
25	309.8	17.2	986	10	AL536160	AL536160
26	309.6	17.2	597	10	AW308961	AW308961 sf92d04.y
27	308.4	17.1	998	10	AL555361	AL555361
28	305	16.9	910	10	AL546378	AL546378
29	298.8	16.6	722	11	BG914796	BG914796 602813602
30	298.6	16.6	871	10	BE747628	BE747628 601577573
31	297.2	16.5	413	11	R84189	R84189 16148 Lambd
32	294.6	16.4	806	11	BG755703	BG755703 602716076
C 33	290.6	16.1	1107	13	CNS07B7W	AL437538 T7 end of
34	289.2	16.1	674	10	BE395451	BE395451 601309973
35	287	15.9	799	11	BG678501	BG678501 602626172
36	286.6	15.9	647	10	AA941409	AA941409 LD25539.5
37	286	15.9	687	10	AU138897	AU138897
38	285.8	15.9	605	11	BI097160	BI097160 SCUM75-DS
39	285.8	15.9	631	10	BE325992	BE325992 NF083F01S
40	285.6	15.9	709	11	BG027036	BG027036 602294084
41	285.2	15.8	834	10	BE742797	BE742797 601574414
42	285.2	15.8	947	11	BG366766	BG366766 602455037
C 43	284.6	15.8	1078	13	CNS077A8	AL432438 T3 end of
44	283.8	15.8	1005	10	AL523091	AL523091
45	283.6	15.8	577	10	AW398856	AW398856 EST309356

ALIGNMENTS

RESULT 1	AV560183/c	609 bp	mRNA	EST	07-SEP-2000
LOCUS	AV560183	Arabidopsis thaliana green siliques Columbia	Arabidopsis		
DEFINITION	thaliana cDNA clone SQ13011F 3', mRNA sequence.				
ACCESSION	AV560183				
VERSION	AV560183.1	GI:8731609			
KEYWORDS	EST				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1 (bases 1 to 609)				
AUTHORS	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.				
TITLE	A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries				
JOURNAL	DNA Res. 7, 175-180 (2000)				
MEDLINE	20363093				
COMMENT	Contact: Erika Asamizu The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.				
FEATURES	1..609				
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	/strain="Columbia"				
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	/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"				

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Query Match      33.8%; Score 608; DB 10; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.3e-100;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 gccgttggtgtgtatgagactgcagttgctgttggtgagtagagccgacacaaactc 1140
Db 609 GCCGTTGCTGGTGTATGAGACTGCAGTTGCTGTGGAGTAGAGCGGACAACTC 550

QY 1141 cttacaatgagattttgagattttcgccagattatacaacttcattgcacccaagt 1200
Db 549 CCTTAAATGAGTATTTGAGTATTTGCGCCAGATTATACGCTTCATGTCGACCAAGT 490

QY 1201 cctatggaatttaaacacgcccacaaagatatggagagataaagaacacgttgcgaa 1260
Db 489 CCTATGGAGAATTTAAACACGCCCAAGATATGGAGAGGATAGGAACACGTTGCTGGA 430

QY 1261 caacttgggactaatacacgcacactagctccagtttccagcacacacaccagtcact 1320
Db 429 CAACCTTCGGAGCTAATACACGCACCTAGCTCCAGTTTCAGCACACACACCACTCAAT 370

QY 1321 ctagttttgagacgcccgaagatgacatggagagacaaacacccctgcacnltggagt 1380
Db 369 CGAGTTTTCGACGCGCGGAAGATGACATGGAGACAAACCAACCTCGCATCTGGAGT 310

QY 1381 ggaactgcgaactatgaatcacagtagacagtagatgataaacctcttcattgactca 1440
Db 309 GGAACCTGCACCTTATGATACACAGTAGCAGATGATGATAAACCTCTTCATGGTTACTCA 250

QY 1441 tgcctgtgtggcgcaactacgacagggactctaccggtgaagatgaatggatgacgat 1500
Db 249 TGTCTGTGTGGCGCAACTACGGACAGGACTCTACCGGTGAAGATGAATGCATCAGT 190

QY 1501 aaccagagcagacagtgaaactccatctcattgattaaacacagcttgatgtgtctc 1560
Db 189 AACCAGAGCCAGACGTAATCTCCATCGTCTTAAACACAGCTTGATGTTGTGTCTC 130

QY 1561 ttttgccatataatgtcgcagatttaagaacaagtttaggggaatgaatgattctt 1620
Db 129 TTTTGCCATATCATATGTGCGCAGATTTAGAACACAGTTAGGGGAATGAATGATCTT 70

QY 1621 taatgtttttcagcaaccttttgagttctgtgaaacgcgtgattgattgaacagltga 1680
Db 69 TGATGTTTTTTCAGCAACCTTTTGAGTTCTGTGAAACGCTGCAATTGATTAGAACAGTGA 10

QY 1681 caactgact 1689
Db 9 CAACGTGACT 1

RESULT 2
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LOCUS
DEFINITION 701498504 A. thaliana, Ohio State clone set Arabidopsis thaliana
ACCESSION A1994522
VERSION A1994522.1 GI:5841427
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 553)
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrigha, A., Murty, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.

```

```

TITLE Arabidopsis thaliana Gene Expression MicroArray
JOURNAL Unpublished (1999)
COMMENT Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
FEATURES
source Location/Qualifiers
1..553
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="701498504"
/clone.lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
BASE COUNT 125 a 129 c 141 g 158 t
ORIGIN

Query Match      28.3%; Score 509.2; DB 10; Length 553;
Best Local Similarity 97.1%; Pred. No. 1.6e-82;
Matches 540; Conservative 0; Mismatches 13; Indels 3; Gaps 2;

QY 313 cgccttagcctgcgtgcgcctccgatatcgccgattccattcgccgagtagttgac 372
Db 1 CGCCCTAGCCTCGCTGAGCCCTCCGATATCGGCCGATTCATTCCGCCGAGTATGTTGAC 60

QY 373 ttctcgtcttcgttccgcccgaatctatggcgatccttcgcgtgcacaaacctaaag 432
Db 61 TTCCTCGCTTCGGTTTCGCCGAATCTATGGCGATCTTCGCTGCAGCAAACTAAGG 120

QY 433 cgattcaatgicggtgagattgctctgtcttcgaagaccttttgcattttgacctgct 492
Db 121 CGATTCAATGTCGGTGAGGATTCCTGCTTCGACGGAATTTTGTGATTTTTCGCGTCT 180

QY 493 tccgcggaggttctattggtgctgcgcgtcaaatataacacagagcgctgatatcgt 552
Db 181 TCCGCCGAGGTTCTATTGGTGTGCTGCCGTCAATTAACACAGACGAGCTGATATCGCT 240

QY 553 atcaattggcggtggtggttcacatgcttaagaaagcgaggtcttgggttttgcatt 612
Db 241 ATCAATTGGGGCTGTGGGCTTCACCATGCTAAAGAAAGCGAGGCTTCTGGGTTTGTCTAT 300

QY 613 gtaaacacatcgtctagagattctgagttgctcaagatttttaacgaggttctctac 672
Db 301 GTAAACACATCTGCTAGGAGTTCTGGAGTTGCTCAAGATGTTTAAGCGGTTCTCTAC 360

QY 673 atagattatgattccaccatggagatggagtggaagaagcgcttttacaccactgata 732
Db 361 ATAGATATTGATGCCACCATGGAGATGGAGTGGAGAGAGCGTTTACACCACTGATAGA 420

QY 733 gttatgactgtttttccacaaatttggggaacttttccacaggaactggtcacataaga 792
Db 421 GTTATGACTGTGTTTTCACAAATTTGGGGG--CTCTTTCCAGGAACCTGTCACATAGA 478

QY 793 gatgttgctgaaaaaggaatactatgctctaaatgttccactaaacagatggtatg 852
Db 479 CATGTTCCGCTGAAAAGGGAATACTACTGCTCTTAATG--TCCACTAAACGATGGTATG 537

QY 853 gacgatgaaagtctcc 868
Db 538 GACGATGAAAGTTCCTCC 553

RESULT 3
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LOCUS
DEFINITION B1177518 737 bp mRNA EST 09-JUL-2001
B1177518 EST518463 CSTE Solanum tuberosum cDNA clone cSTE10D9 5' sequence.
B1177518 mRNA sequence.
ACCESSION B1177518
VERSION B1177518.1 GI:14643329

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414	QY	cgctgcacaaacctaaaggcgattcaatgtcggtaggaattctctgtcttcgcgcgact	473
274	Db	C-----AACGACATCGAGAGATTCAACGTTGGTAGGACTGCTCCAGTATTCCGATGGCT	327
474	QY	ttttgatttttgcgcgtcttcgcgcggaggtttctattggtcgtcgcgtcaaatataacag	533
328	Db	GTTTGAGTCTGTGCAGTTGTCTACTGGTGGTTCTGTGSCAACTGCTGTGAACCTTAATAA	387
534	QY	acaggacgctgatatcgcctatcaattggcgcggtggggttcaccatgctcaagaaagcga	593
388	Db	GCAGCAGACGGACATCGCTGCAATTTGGCTGGGGGCTGCACCATGCAAGAAGCTCCGA	447
594	QY	ggcttctgggttttgctatgtaaacgacatcgctcagggaattctggagttgctcaaat	653
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654	QY	gttaagcgggttctctacatagatatgatgcccaccatggagatggagtggaagaagc	713
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714	QY	gtttacaccactgataaagattatcagctgtttcttccacaaaatttggggacttttccc	773
568	Db	CTTCTACACACGGACCGGGTGCATGACGTGTGCTTTTCATAAGTATGGAGAGTACTTCCC	627
774	QY	aggaactggctacataaagagatgttggcgcgtgaaaaagggaaatactactgctctaaatgt	833
628	Db	AGGAACGTGGGACCTACGGGATATCGGGCTGGCAAGCAAGTATTATGCTGTTAATA	687
834	QY	tccactaaacgattgtagaacgatgaaagtttccgcagcttgtttagacccttattcca	893
688	Db	CCCSCTCCSAGACGGGATTGATGACGAGTCCCTATTGAGGCCATTTTCAAGCCGGTCATGTC	747
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748	Db	CAAAAGTAATGGAGATGTTCCASCCTTAGTGGGGTCTTACAGTGTGGCTCAGACTCCCT	807
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Job time: 1449 sec